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PCT 8

RAW SEQUENCE LISTING DATE: 12/26/2000  
PATENT APPLICATION: US/09/700,293 TIME: 13:14:21

Input Set : A:\seqlist.txt  
Output Set: N:\CRF3\12262000\I700293.raw

4 <110> APPLICANT: SmithKline Beecham Biologicals  
5 Rhelle, Jean-Louis  
7 <120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides  
8 from Neisseria Meningitidis  
11 <130> FILE REFERENCE: BM15321  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/700,293  
C--> 13 <141> CURRENT FILING DATE: 2000-11-13  
13 <150> PRIOR APPLICATION NUMBER: PCT/EP99/03255  
14 <151> PRIOR FILING DATE: 1999-05-07  
16 <150> PRTOR APPLICATION NUMBER: GB 9810276.7  
17 <151> PRIOR FILING DATE: 1998-05-13  
19 <160> NUMBER OF SEQ ID NOS: 6  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1785  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Bacteria  
28 <400> SEQUENCE: 1  
29 atgaaacaaaa tataccgcatt catttggaaat agtgccttcata tgccgttgggt cggcgtatcc 60  
30 gagctccacacac gcaacgcggcc ttccgaacacgg tggcgaccgc cgtatggcg 120  
31 acactgttgtt ttgcacacggtt tcaggccqagt actacccqatg acgcgattttt atattttagaa 180  
32 cccgtacaaac gcaactgttgtt ctgttggac ttccgttccg ataaagaagg cacgggagaaa 240  
33 aaagaagttt cagaagattt aatttggggaa gtatattttcg acaagaaggagg agtactaaca 300  
34 qccggaaacaa tccccctcaaa agccggcgac aacctggaaaa tcaaacaaaa caccatggaa 360  
35 aacaccaatgtt ccacgttactcg ctggaaaaaaag accttcacaga tctggaccgt 420  
36 gtttggacty taaaattttttt gttttagcccaaa aacgcacataa aagtccacat cacaaggcgac 480  
37 accaaaaggctt tggattttccg gaaaaaaacg qcttgagaccac acggcgacac cacgggttcat 540  
38 ctgaacggta tccgttgcac ttttgcggat acgtctgttgc ataccggayc gaccacaaac 600  
39 gtaacccaaacg acaacacgttccg acgtacggag aaaaaacgttccg cggcggccgtt taagacgtt 660  
40 tttaaacccggcgtt taaaaggccgtt aaacccggta caacacgttccg cgtataacgtt 720  
41 gatlttcgttcc gcaacttacgca ccaacttcggat ttcttgcgttccg cagatccaa aacaacgact 780  
42 gtttaatgtgg aayccaaaggaa caarccggcaacgg agaaccggaa tttaaatccgg tccggaaatgtt 840  
43 tctgttatca aagaaaaaggaa cggtaagggtt gttacttggta aagacaaagg cgagaatgtt 900  
44 tcttctacag acaaaggccgaa aggctttagtgc actqccaaaagg aagtgttgc tccgttacaaac 960  
45 aqggctgggtt qgaaatggaa aacaacaaacc gctaattggtc aacacgggtcc acgttgcggaa 1020  
46 ttttggaaaccgg tttacatccgg cacaatgttca accltttgcgtt gttgttggaaatgg tttacactcg 1080  
47 actgttaatgttccg aagatgttca acggccacatc actgttgcgtt atgtatgttgc tccgttgcgtt 1140  
48 gcccattaaacg tcaatccggat gcaaaacacgg ggttggaaattt tggattccaa acgggttgc 1200  
49 gtttcttccgg qcaaaaggccat cagccggccat qtttccggccg gcaaggggaaa gatggatggaa 1260  
50 accglcaaca ttaatccggcc caacaacatc gagalltccg gcaacccggaa aataatccggac 1320  
51 atccggccactt cgtatggccccc gcaatthtttccg acgttgcgttcc tccggccgggg ggccggatgttccg 1380  
52 ccccaatllaa ggggttggatca cggggccggcc gttaaatgttccg gcaacccggaa tccggccaaatggaa 1440  
53 cccgtccggca ttaccaatgttccg cggccggccg gttaaatgttccg gggatgttac aacacgttgc 1500  
54 caacttaaaggccgttggccgaa aacatgttgcac aaccacatc gcaatgttgc gggccaaatggcc 1560  
55 cggccggccgca tccggccaaatggccg gttttccggccg gttaaatgttccg gggatgttac aacacgttgc 1620  
56 aagatgtatgttccg gggccggccg tttccggccgaa aacccgggttccg tcccatccggcc 1680  
57 tactcaaaatggccgaaatgttccg gggaaatgttccg aatccggccgaaatgttccg gggccaaatggcc 1740

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Input Set : A:\seqlist.txt  
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 60 <210> SEQ ID NO: 2  
 61 <211> LENGTH: 594  
 62 <212> TYPE: PRT  
 63 <213> ORGANISM: Bacteria  
 65 <400> SEQUENCE: 2  
 66 Met Asn Lys Ile Tyr Arg Ile Ile Trp Asn Ser Ala Leu Asn Ala Trp  
 67 1 5 10 15  
 68 Val Ala Val Ser Glu Leu Thr Arg Asn His Thr Lys Arg Ala Ser Ala  
 69 20 25 30  
 70 Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln  
 71 35 40 45  
 72 Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg  
 73 50 55 60  
 74 Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu  
 75 65 70 75 80  
 76 Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys  
 77 85 90 95  
 78 Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu  
 79 100 105 110  
 80 Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr  
 81 115 120 125  
 82 Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu  
 83 130 135 140  
 84 Lys Leu Ser Phe Ser Ala Asn Ser Asn Lys Val Asn Ile Thr Ser Asp  
 85 145 150 155 160  
 86 Thr Lys Gly Leu Asn Phe Ala Lys Lys Thr Ala Glu Thr Asn Gly Asp  
 87 165 170 175  
 88 Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu  
 89 180 185 190  
 90 Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp  
 91 195 200 205  
 92 Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly  
 93 210 215 220  
 94 Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val  
 95 225 230 235 240  
 96 Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr  
 97 245 250 255  
 98 Lys Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr  
 99 260 265 270  
 100 Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly  
 101 275 280 285  
 102 Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Asp Ser Ser Thr Asp  
 103 290 295 300  
 104 Lys Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn  
 105 305 310 315 320  
 106 Lys Ala Gly Trp Arg Met Lys Thr Thr Ala Asn Gly Gln Thr Gly  
 107 325 330 335  
 108 Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe.

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109	340	345	350	
110 Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly				
111	355	360	365	
112 Asn Ile Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val				
113	370	375	380	
114 Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala				
115	385	390	395	400
116 Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly				
117	405	410	415	
118 Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile				
119	420	425	430	
120 Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln				
121	435	440	445	
122 Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser				
123	450	455	460	
124 Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Asp Ala Asn Lys				
125	465	470	475	480
126 Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val				
127	485	490	495	
128 Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His				
129	500	505	510	
130 Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile				
131	515	520	525	
132 Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met				
133	530	535	540	
134 Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly				
135	545	550	555	560
136 Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala				
137	565	570	575	
138 Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr				
139	580	585	590	
140 Gln Trp				
143 <210> SEQ ID NO: 3				
144 <211> LENGTH: 1776				
145 <212> TYPE: DNA				
146 <213> ORGANISM: Bacteria				
148 <400> SEQUENCE: 3				
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150 gagctcacac gcaaccacac caaacgcgcc tcgcgaacctc tgaagacgcgc cgtattggcg			120	
151 acactqttgt ttgcacacqgt tcaggcaaqgt gctaacaatg aagagaacaaga agaagattta			180	
152 tatttagacc ccgtacaacg cactgttgcc gtgttgatag tcaattccca taaaagaaggc			240	
153 acgggagaaa aagaaaaagt agaaaaaaat tcgatgggg cagtatattt caacgagaaa			300	
154 ggagttactaa caqccagaga aatccccctc aaagccggcg acaacctgaa aatcaaacaacaa			360	
155 aacggccacaa acttcacccia ctgcgtgaaa aaagacccctca cagatctgac caglgttgaa			420	
156 actgaaaaat ttcgttttag cgcaaacggc aataaagtca acatccacaag cgacacccaaa			480	
157 ggcttggatt ttgcgaaaga aacgctggg acgaaacggcg acaccacgggt tcacctgaaac			540	
158 ggatgttgtt cgactttgac cgatacgctg ctgaataccg gagcgaccac aaacgttaacc			600	
159 aacgacaacg ttaccgatga cgaaaaaaa cgtgcggcaa gcgttaaaga cgttaaaac			660	
160 gcaggctgga acattaaagg ctttaacccc ygtacaaacag cttccgataa cgttgatttc			720	

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161	gtccgcactt	acgacacagt	cgagltcttg	agcgcagata	cgaaaacaac	gacttttaat	780
162	gttggaaagca	aagacaaacgg	caagaaaaacc	gaatgtlaaaa	tgggtgcgaa	gacttcgtt	840
163	attuuagaaa	a3qacggtaa	qtttgttact	ggttaaagaca	aaggcggaaa	tgqtltctt	900
164	acagacyaag	qcgaaaggctt	agtgtactgca	aaaqaagtga	ttgtatgcgt	aaacaqaqct	960
165	qgtfrggagaa	tqaaaacaac	aaccgcataat	ggtcaaacq	gtcaagctga	caayttqaa	1020
166	accgttacat	caggcataaaa	tgttacccctt	gctgttggtt	aagglaacaac	tgcgactgt	1080
167	atgtuaaqatg	atcaaaqcacaa	catactgtt	atgtatgtt	taaatgtcqy	cgtatcccata	1140
168	aacgtcaatc	agctgcaaaa	caqrggttgg	aattttgtttt	ccaaagcggt	tgcaggtrct	1200
169	tctggcaaaag	tcatcagcgg	caatgtttcg	ccgagcaayg	gauagatgya	tgaaaccgtc	1260
170	aacattaaatg	ccggcaacaa	catcgagattt	acccycaacg	gtaaaaalal	cgacalccgac	1320
171	acttcgatgt	ccccgcgtt	tccagcggtt	tcqclcgcc	cyggggccgg	tgcqcccact	1380
172	tttgcgttgg	atqqqgacgc	atqaaatgtc	ggcagcaaga	ggacaaacaa	acccytccqc	1440
173	attaccaatg	tcccccgggg	cytttaaagg	qgggatgtt	caacacgtgc	acaacttaaa	1500
174	ggcggtggcgc	aaauacttqaa	caaccyccatc	qacaatgtgg	acggcaacgc	ycgtqcgqgc	1560
175	atcgccccaaq	cgatttgcac	cycaggctt	gttgcggcgt	atttgcggg	caagagtatq	1620
176	atggcgtatcg	qcgggcggcac	ttaatgcggc	qaagcccggtt	acggccatcg	ctactccagt	1680
177	atttccgacg	qcgggaaattt	gattatcaa	ggcactggctt	ccggcaatte	ycgeggccat	1740
178	ttcgatgttt	ccgcacatgt	cggttatacg	tgttaa			1776

180 <210> SEQ ID NO: 4

181 <211> LENGTH: 591

182 <212> TYPE: PRT

183 <213> ORGANISM: Bacteria

185 <400> SEQUENCE: 4

186	Met	Asn	Lys	Ile	Tyr	Arg	Ile	Ile	Trp	Asn	Ser	Ala	Leu	Asn	Ala	Trp
187	1			5			10		15							
188	Val	Ala	Val	Ser	Glu	Leu	Thr	Arg	Asn	His	Thr	Lys	Arg	Ala	Ser	Ala
189							20		25							30
190	Thr	Val	Lys	Thr	Ala	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ala	Thr	Val	Gln
191							35		40							45
192	Ala	Ser	Ala	Asn	Asn	Glu	Glu	Gln	Glu	Glu	Asp	Leu	Tyr	Leu	Asp	Pro
193							50		55							60
194	Val	Gln	Arg	Thr	Val	Ala	Val	Leu	Ile	Val	Asn	Ser	Asp	Lys	Glu	Gly
195	65						65		70							80
196	Thr	Gly	Glu	Lys	Glu	Lys	Val	Glu	Glu	Asn	Ser	Asp	Trp	Ala	Val	Tyr
197							85		90							95
198	Phe	Asn	Glu	Lys	Gly	Val	Leu	Thr	Ala	Arg	Glu	Ile	Thr	Leu	Lys	Ala
199							100		105							110
200	Gly	Asp	Asn	Leu	Lys	Ile	Lys	Gln	Asn	Gly	Thr	Asn	Phe	Thr	Tyr	Ser
201							115		120							125
202	Leu	Lys	Lys	Asp	Leu	Thr	Asp	Leu	Thr	Ser	Val	Gly	Thr	Glu	Lys	Leu
203							130		135							140
204	Ser	Phe	Ser	Ala	Asn	Gly	Asn	Lys	Val	Asn	Ile	Thr	Ser	Asp	Thr	Lys
205	145						145		150							160
206	Gly	Leu	Asn	Phe	Ala	Lys	Glu	Thr	Ala	Gly	Thr	Asn	Gly	Asp	Thr	Thr
207							165		170							175
208	Val	His	Leu	Asn	Gly	Ile	Gly	Ser	Thr	Leu	Thr	Asp	Thr	Leu	Leu	Asn
209							180		185							190
210	Thr	Gly	Ala	Thr	Thr	Asn	Val	Thr	Asn	Asp	Asn	Val	Thr	Asp	Asp	Glu
211							195		200							205

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212 Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn  
 213 210 215 220  
 214 Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe  
 215 225 230 235 240  
 216 Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr  
 217 245 250 255  
 218 Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val  
 219 260 265 270  
 220 Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu  
 221 275 280 285  
 222 Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly  
 223 290 295 300  
 224 Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala  
 225 305 310 315 320  
 226 Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala  
 227 325 330 335  
 228 Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser  
 229 340 345 350  
 230 Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile  
 231 355 360 365  
 232 Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln  
 233 370 375 380  
 234 Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser  
 235 385 390 395 400  
 236 Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met  
 237 405 410 415  
 238 Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg  
 239 420 425 430  
 240 Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser  
 241 435 440 445  
 242 Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser Val Asp  
 243 450 455 460  
 244 Gly Asp Ala Leu Asn Val Gly Ser Lys Lys Asp Asn Lys Pro Val Arg  
 245 465 470 475 480  
 246 Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val Thr Asn Val  
 247 485 490 495  
 248 Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn Arg Ile Asp Asn  
 249 500 505 510  
 250 Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile Ala Thr Ala  
 251 515 520 525  
 252 Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met Ala Ile Gly  
 253 530 535 540  
 254 Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly Tyr Ser Ser  
 255 545 550 555 560  
 256 Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala Ser Gly Asn  
 257 565 570 575  
 258 Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr Gln Trp  
 259 580 585 590  
 261 <210> SEQ ID NO: 5

VERIFICATION SUMMARY DATE: 12/26/2000  
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Input Set : A:\seqlist.txt  
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date